#6 PK

RAW SEQUENCE LISTING   DATE: 01/23/2002
PATENT APPLICATION: US/09/830,524   TIME: 17:43:16

Input Set : A:\Neuro431.app
Output Set: N:\CRF3\01232002\I830524.raw

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 3 <110> APPLICANT: Tao, Weng
 4           Wong, Shou
 5           Hickey, William F
 6           Hammang, Joseph P
 7           Baetge, Edward E
 9 <120> TITLE OF INVENTION: Cell Surface Molecule-Induced Macrophage Activation
11 <130> FILE REFERENCE: 19141-543NATL
13 <140> CURRENT APPLICATION NUMBER: 09/830,524
14 <141> CURRENT FILING DATE: 2001-04-26
16 <150> PRIOR APPLICATION NUMBER: PCT/US99/24630
17 <151> PRIOR FILING DATE: 1999-10-21
19 <150> PRIOR APPLICATION NUMBER: 09/178,869
20 <151> PRIOR FILING DATE: 1998-10-26
22 <160> NUMBER OF SEQ ID NOS: 14
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1019
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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34 gtggagatga aacttgctgt agatgaagaa gaaaatgctg acaataacac aaaggccaat 180
35 gtcacaaaac caaaaaggtg tagtggaagt atctgctatg ggactattgc tgtgatcgtc 240
36 tttttcttga ttggatttat gattggctac ttgggctatt gtaaaggggt agaaccaaaa 300
37 actgagggat ccgagcccaa atcttgtgac aaaactcaca catgcccacc gtgcccagca 360
38 cctgaactcc tggggggacc gtcagtcttc ctcttccccc caaaacccaa ggacaccctc 420
39 atgatctccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 480
40 gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 540
41 cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 600
42 gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct cccagccccc 660
43 atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg 720
44 cccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc 780
45 ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac 840
46 aagaccacgc ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc 900
47 gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 960
48 ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaatg aagcttggg 1019
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52 <211> LENGTH: 331
53 <212> TYPE: PRT
54 <213> ORGANISM: Homo sapiens
56 <400> SEQUENCE: 2
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60  Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp
61           20                 25                30
63  Asn Ser His Val Glu Met Lys Leu Ala Val Asp Glu Glu Glu Asn Ala
64           35                 40                45
66  Asp Asn Asn Thr Lys Ala Asn Val Thr Lys Pro Lys Arg Cys Ser Gly
67       50                 55                60
69  Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly
70  65               70                75                80
72  Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr
73               85                90                95
75  Glu Gly Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
76           100                105                110
78  Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
79           115                120                125
81  Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
82       130                135                140
84  Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
85  145               150                155                160
87  Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
88               165                170                175
90  Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
91           180                185                190
93  Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
94           195                200                205
96  Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
97       210                215                220
99  Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
100 225                230                235                240
102 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
103           245                250                255
105 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
106           260                265                270
108 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
109       275                280                285
111 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
112       290                295                300
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118           325                330
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122 <211> LENGTH: 974
123 <212> TYPE: DNA
124 <213> ORGANISM: Homo sapiens
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128 gaaccattgt catatacccg gttcagcctg gctcggcaag tagatggcga taacagtcat 120
129 gtggagatga aacttgctgt agatgaagaa gaaaatgctg acaataacac aaaggccaat 180
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131 tttttcttga ttggatttat gattggctac ttgggctatt gtaaaggggt agaaccaaaa 300
132 actgagggat ccgcacctga actcctgggg ggaccgtcag tcttcctctt ccccccaaaa 360
133 cccaaggaca ccctcatgat ctcccggacc cctgaggtca catgcgtggt ggtggacgtg 420
134 agccacgaag accctgaggt caagttcaac tggtacgtgg acggcgtgga ggtgcataat 480
135 gccaagacaa agccgcggga ggagcagtac aacagcacgt accgtgtggt cagcgtcctc 540
136 accgtcctgc accaggactg gctgaatggc aaggagtaca agtgcaaggt ctccaacaaa 600
137 gccctcccag cccccatcga gaaaaccatc tccaaagcca agggcagcc ccgagaacca 660
138 caggtgtaca ccctgccccc atcccgggat gagctgacca gaaccaggt cagcctgacc 720
139 tgcctggtca aaggcttcta tcccagcgac atcgccgtgg agtgggagag caatgggcag 780
140 ccggagaaca actacaagac cacgcctccc gtgctggact ccgacggctc cttcttcctc 840
141 tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgctcc 900
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153  1               5                  10                  15
155 Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp
156              20                  25                  30
158 Asn Ser His Val Glu Met Lys Leu Ala Val Asp Glu Glu Glu Asn Ala
159          35                  40                  45
161 Asp Asn Asn Thr Lys Ala Asn Val Thr Lys Pro Lys Arg Cys Ser Gly
162       50                  55                  60
164 Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly
165  65                  70                  75                  80
167 Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr
168                  85                  90                  95
170 Glu Gly Ser Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
171             100                 105                 110
173 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
174             115                 120                 125
176 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
177       130                 135                 140
179 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
180 145                 150                 155                 160
182 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
183                 165                 170                 175
185 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
186             180                 185                 190
188 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
189          195                 200                 205
191 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
192          210                 215                 220
194 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
195 225                 230                 235                 240
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197 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
198                 245                 250                 255
200 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
201                 260                 265                 270
203 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
204             275                 280                 285
206 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
207         290                 295                 300
209 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 305                 310                 315
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218 <220> FEATURE:
219 <223> OTHER INFORMATION: Description of Artificial Sequence:
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227 <211> LENGTH: 33
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229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence:
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235 <400> SEQUENCE: 6
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240 <211> LENGTH: 32
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: Description of Artificial Sequence:
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248 <400> SEQUENCE: 7
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270 <220> FEATURE:
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309 <220> FEATURE:
310 <223> OTHER INFORMATION: Description of Artificial Sequence:
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317 <210> SEQ ID NO: 13
318 <211> LENGTH: 32
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
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323 <223> OTHER INFORMATION: Description of Artificial Sequence:
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326 <400> SEQUENCE: 13
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332 <212> TYPE: DNA
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336 <223> OTHER INFORMATION: Description of Artificial Sequence:
337      Oligonucleotide primer
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VERIFICATION SUMMARY
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